

## SEQUENCE LISTING

<110> Gozes, Illana  
Brenneman, Douglas E.  
Bassan, Merav  
Zamostiano, Rachel  
The Government of the United States of America  
as represented by the Secretary of the  
Department of Health and Human Services

<120> Activity Dependent Neurotrophic Factor III (ADNF III)

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<151> 1997-02-07

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<170> PatentIn Ver. 2.0

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 ctaggtttta acatgaaaga attaaataaa gtcaaacacg agatggattt tgatgctgag 1620  
 tggctgtttg aaaatcacga tgagaaagac tcaagagtca atgctagcaa gactgttgac 1680  
 aaaaagcata accttgggaa agaagatgat agcttctcag atagttttga acatttggaa 1740  
 gaagaatcca atggaagcgg gagtctttt gaccctgtct ttgaagttga gcctaaaatt 1800  
 cccagtgata atttagagga gcctgtaccg aaggttattc cggaagggtgc tttggaatct 1860  
 gagaagctag accaaaaaga ggaggaggag gaggaggagg aggaggatgg ttcaaaatat 1920  
 gaaactatcc atttgactga ggaaccagcc aaattaatgc atgatgcctc tgatagttag 1980  
 gtagaccaag atgatgtagt tgagtggaaa gatggtgctt caccatctga gagtgggcct 2040  
 ggttcccaac aaatctcaga ctttgaggat aatacatgtg aaatgaaacc aggaacctgg 2100  
 tctgatgagt cttcccagag tgaagatgca aggagcagta agccagctgc caaaaaaag 2160  
 gctacagtgc aagatgacac agagcagtta aaatggaaga atagttccta tggaaaagtt 2220  
 gaagggtttt ggtccaagga ccagtcacag tgggaaaatg catctgagaa tgcagagcgc 2280  
 ttaccaaacc cacagattga gtggcagaat agcacaattg acagtgagga cggggagcag 2340  
 tttgacagca tgactgacgg agttgctgat cccatgcatg gcagcttaac tggagtgaag 2400

ctgagcagcc agcaagcctg a

2421

<210> 5  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:ADNF-9 active  
 peptide antigen

<400> 5  
 Ser Ala Leu Leu Arg Ser Ile Pro Ala  
 1 5

<210> 6  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:ADNF III-8  
 active site core peptide, clone 25 sequence (NAP)

<400> 6  
 Asn Ala Pro Val Ser Ile Pro Gln  
 1 5

<210> 7  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:sense primer  
 for amplification of ADNF III cDNA

<400> 7  
 tccaatgttc acctgcag

18

<210> 8  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:antisense  
 primer (bases 438-455) for amplification of ADNF  
 III cDNA

<400> 8  
 gctcgttaca gattgtac

18

<210> 9  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:sense primer  
 (bases 71-90) for amplification of ADNF III cDNA

<400> 9  
 acctgcagca aaacaactat

20

<210> 10  
 <211> 88  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:activity  
 dependent neurotrophic factor III (ADNF III)  
 polypeptide

<220>  
 <221> MOD\_RES  
 <222> (1)..(40)  
 <223> Xaa = any amino acid, Xaa at positions 1-40 may be  
 present or absent

<220>  
 <221> MOD\_RES  
 <222> (49)..(88)  
 <223> Xaa = any amino acid, Xaa at positions 49-88 may be  
 present or absent

<400> 10  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 1 5 10 15  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 20 25 30  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Ala Pro Val Ser Ile Pro Gln  
 35 40 45  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 50 55 60  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 65 70 75 80  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 85

<210> 11  
 <211> 5  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:short hsp60  
homolog control peptide

<400> 11

Leu Gly Gly Gly Ser  
1 5

<210> 12

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III  
polypeptide

<400> 12

Ser Val Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln  
1 5 10 15

Gln Ser

<210> 13

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III  
polypeptide; short hsp60 homolog control peptide

<400> 13

Val Leu Gly Gly Gly  
1 5

<210> 14

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III  
polypeptide

<400> 14

Val Leu Gly Gly  
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<210> 15

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III  
polypeptide

<400> 15

Val Leu Gly Gly Val  
1 5

<210> 16

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III  
polypeptide

<400> 16

Gly Val Leu Gly Gly  
1 5

<210> 17

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III  
polypeptide

<400> 17

Leu Gly Leu Gly Gly  
1 5

<210> 18

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF III  
polypeptide

<400> 18

Ser Val Arg Leu Gly Leu Gly Gly  
1 5

<210> 19

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:related to  
yeast protein PIF1



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<220>  
<221> MOD_RES  
<222> (10)  
<223> Xaa = unknown
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<210> 20
<211> 13
<212> PRT
<213> Artificial Sequence
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<220>
<221> MOD_RES
<222> (5)
<223> Xaa = unknown
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<220>  
<221> MOD_RES  
<222> (10)  
<223> Xaa = unknown
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<210> 21
<211> 15
<212> PRT
<213> Artificial Sequence
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<400> 21  
Cys Val Leu Gly Gly Gly Ser Ala Leu Leu Arg Ser Ile Pro Ala  
1 5 10 15

<210> 22  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:peptide  
 conjugated through the Cys residue to Sephadex for  
 affinity chromatography

<400> 22  
 Cys Ser Ala Leu Leu Arg Ser Ile Pro Ala  
     1                    5                    10

<210> 23  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:active peptide  
 of ADNF I hsp60-related sequence

<400> 23  
 Val Leu Gly Gly Gly Ser Ala Leu Leu Arg Ser Ile Pro Ala  
     1                    5                    10

<210> 24  
 <211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:hsp60 homolog  
 peptide

<400> 24  
 Val Leu Gly Gly Gly Cys Ala Leu Leu Arg Cys Ile Pro Ala  
     1                    5                    10

<210> 25  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:mimic hybrid  
 primer

<400> 25  
 acctgcagca aaacaactat tttccatccc tcaacagt

38

<210> 26  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cyclophilin  
mRNA upper primer, position 348

<400> 26

atggcacagc aggaaagagc

20

<210> 27

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cyclophilin  
mRNA lower primer

<400> 27

ttgccggagt cgacaatgat

20

<210> 28

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:sequence of p25  
clone with structural similarity to active peptide  
of ADNF I

<400> 28

Gly Gly Asn Ala Pro Val Ser Ile Pro

1

5

<210> 29

<211> 837

<212> DNA

<213> Homo sapiens

<220>

<223> PCR of human ADNF III cDNA from human  
neuroblastoma, sense

<400> 29

cattggggccg acgtgcgatg ctcccgcccg ccattggccgc gggattacct gcagcaaac 60

aactatggag tcaaattctgt aggccagggt tacagtgttg gtcagtcaat gagactgggt 120

ctaggtggca acgcaccagt ttccattcct caacaatctc agtctgtaaa gcagttactt 180

ccaagtggaa acggaaggtc ttatgggctt gggtcagagc agaggtccca ggcaccagca 240

agatactccc tgcagtctgc taatgcctct tctctctcat cgggccagtt aaagtctcct 300

tccctctctc agtcacaggc atccagagtg ttaggtcagt ccagttccaa acctgctgca 360

gctgccacag gccctcccc aggtaacct tctcaactc aaaagtggaa aatatgtaca 420

atctgtaacg agcaatcact agtgcggccg cctgcaggtc gaccatatgg gagagctccc 480

aacgcgttgg atgcatagct tgagtattct atagtgtcac ctaaataget tggcgtaatc 540  
 atggtcatag ctgtttcctg tgtgaaattg ttatccgctc acaattccac acaacatacg 600  
 aaccggaagc ataaagtgtg aagcctgggg tgcctaataga atgagctaac tcacattaat 660  
 tgcgttgccg tcactgcccg ctttccaatc nggaaactgt cgtgccaaact gcattaatga 720  
 atcgccaac gcgcggggaa aagcggtttg cgtattgggc gctcttcgcg ttctcgctc 780  
 aatgaatccc tgcgctcngt ccttccgntg cggnaacgg tatcactcac tcaatt 837

<210> 30

<211> 850

<212> DNA

<213> Homo sapiens

<220>

<223> PCR of human ADNF III cDNA from human  
neuroblastoma, antisense

<400> 30

atnnatatca agctatgcat ccaacgcgtt gggagctctc ccatatggtc gacctgcagg 60  
 cggccgcact agtgattgct cgttacagat tgtacatatt ttccactttt gagttgagga 120  
 agtgttacct gggggagggc ctgtggcagc tgcagcaggt ttggaactgg actgacctaa 180  
 cactctggat gcctgtgact gagagagggg aggagacttt aactggcccg atgagagaga 240  
 agaggcatta gcagactgca gggagtatct tgctgggtgcc tgggacctct gctctgacct 300  
 aagcccataa gaccttccgt ttccacttgg aagtaactgc ttacagact gagattgttg 360  
 aggaatggaa actggtgcgt tgccacctag acccagtctc attgactgac caacactgta 420  
 accctggcct acagatttga ctccatagtt gttttgctgc aggtaatccc gcggccatgg 480  
 cggccgggag catgcgacgt cgggcccgaat tcgcctata gtgagtcgta ttacaattca 540  
 ctggccgtcg ttttacaacg tcgtgactgg gaaaaccctg gcgttaccca acttaatccc 600  
 cttgcagcac atcccccttt cgccagctgg cgtaataaac gaagaagccc gcaccgatcg 660  
 cccttcccaa cagttgcgca gcctgaatgg cgaatggacg cgctgttag cgcgcattaa 720  
 accccgcggg tgttgtggtt acgccgcagc gtgaccgcta cacttgccac cccctaacgc 780  
 ccgctccttt ccctttcttc cttcctttct cgccacgtcc cccgntttcc ccgtccaact 840  
 ctaaatacgg 850

<210> 31

<211> 787

<212> PRT

<213> Mus musculus

&lt;220&gt;

<223> mouse activity dependent neurotrophic factor III  
(ADNF III)

&lt;400&gt; 31

Met	Ser	Asn	Val	His	Leu	Gln	Gln	Asn	Asn	Tyr	Gly	Val	Lys	Ser	Val
1				5					10					15	

Gly	Gln	Ser	Tyr	Gly	Val	Gly	Gln	Ser	Val	Arg	Leu	Gly	Leu	Gly	Gly
			20					25					30		

Asn	Ala	Pro	Val	Ser	Ile	Pro	Gln	Gln	Ser	Gln	Ser	Val	Lys	Gln	Leu
		35					40					45			

Leu	Pro	Ser	Gly	Asn	Gly	Arg	Ser	Phe	Gly	Leu	Gly	Ala	Glu	Gln	Arg
	50					55					60				

Pro	Pro	Ala	Ala	Ala	Arg	Tyr	Ser	Leu	Gln	Thr	Ala	Asn	Thr	Ser	Leu
65					70					75					80

Pro	Pro	Gly	Gln	Val	Lys	Ser	Pro	Ser	Val	Ser	Gln	Ser	Gln	Ala	Ser
				85					90					95	

Arg	Val	Leu	Gly	Gln	Ser	Ser	Ser	Lys	Pro	Pro	Pro	Ala	Ala	Thr	Gly
		100						105					110		

Pro	Pro	Pro	Ser	Asn	His	Cys	Ala	Thr	Gln	Lys	Trp	Lys	Ile	Cys	Thr
		115					120					125			

Ile	Cys	Asn	Glu	Leu	Phe	Pro	Glu	Asn	Val	Tyr	Ser	Val	His	Phe	Glu
	130					135					140				

Lys	Glu	His	Lys	Ala	Glu	Lys	Val	Pro	Ala	Val	Ala	Asn	Tyr	Ile	Met
145					150					155					160

Lys	Ile	His	Asn	Phe	Thr	Ser	Lys	Cys	Leu	Tyr	Cys	Asn	Arg	Tyr	Leu
			165						170					175	

Pro	Thr	Asp	Thr	Leu	Leu	Asn	His	Met	Leu	Ile	His	Gly	Leu	Ser	Cys
		180						185					190		

Pro	Tyr	Cys	Arg	Ser	Thr	Phe	Asn	Asp	Val	Glu	Lys	Met	Ala	Ala	His
		195					200					205			

Met	Arg	Met	Val	His	Ile	Asp	Glu	Glu	Met	Gly	Pro	Lys	Thr	Asp	Ser
	210					215					220				

Thr	Leu	Ser	Phe	Asp	Leu	Thr	Leu	Gln	Gln	Gly	Ser	His	Thr	Asn	Ile
225					230					235					240

His	Leu	Leu	Val	Thr	Thr	Tyr	Asn	Leu	Arg	Asp	Ala	Pro	Ala	Glu	Ser
			245						250					255	

Val	Ala	Tyr	His	Ala	Gln	Asn	Asn	Ala	Pro	Val	Pro	Pro	Lys	Pro	Gln
			260					265					270		

Pro	Lys	Val	Gln	Glu	Lys	Ala	Asp	Val	Pro	Val	Lys	Ser	Ser	Pro	Gln
		275					280					285			

Ala	Ala	Val	Pro	Tyr	Lys	Lys	Asp	Val	Gly	Lys	Thr	Leu	Cys	Pro	Leu
		290				295					300				

Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His His  
 305 310 315 320  
 Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu Lys  
 325 330 335  
 Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn  
 340 345 350  
 Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly Val  
 355 360 365  
 Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu  
 370 375 380  
 Asn Gln Ser Pro Gly Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met  
 385 390 395 400  
 Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Glu Glu Asp Ala Asp Ser  
 405 410 415  
 Pro Ser Cys Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu  
 420 425 430  
 Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe  
 435 440 445  
 Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile  
 450 455 460  
 Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser  
 465 470 475 480  
 His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr  
 485 490 495  
 Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val  
 500 505 510  
 Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp  
 515 520 525  
 Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Val Asp Lys Lys His  
 530 535 540  
 Asn Leu Gly Lys Glu Asp Asp Ser Phe Ser Asp Ser Phe Glu His Leu  
 545 550 555 560  
 Glu Glu Glu Ser Asn Gly Ser Gly Ser Pro Phe Asp Pro Val Phe Glu  
 565 570 575  
 Val Glu Pro Lys Ile Pro Ser Asp Asn Leu Glu Glu Pro Val Pro Lys  
 580 585 590  
 Val Ile Pro Glu Gly Ala Leu Glu Ser Glu Lys Leu Asp Gln Lys Glu  
 595 600 605  
 Glu Glu Glu Glu Glu Glu Glu Glu Asp Gly Ser Lys Tyr Glu Thr Ile  
 610 615 620

His Leu Thr Glu Glu Pro Ala Lys Leu Met His Asp Ala Ser Asp Ser  
 625 630 635 640  
 Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro  
 645 650 655  
 Ser Glu Ser Gly Pro Gly Ser Gln Gln Ile Ser Asp Phe Glu Asp Asn  
 660 665 670  
 Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser  
 675 680 685  
 Glu Asp Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Val  
 690 695 700  
 Gln Asp Asp Thr Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys  
 705 710 715 720  
 Val Glu Gly Phe Trp Ser Lys Asp Gln Ser Gln Trp Glu Asn Ala Ser  
 725 730 735  
 Glu Asn Ala Glu Arg Leu Pro Asn Pro Gln Ile Glu Trp Gln Asn Ser  
 740 745 750  
 Thr Ile Asp Ser Glu Asp Gly Glu Gln Phe Asp Ser Met Thr Asp Gly  
 755 760 765  
 Val Ala Asp Pro Met His Gly Ser Leu Thr Gly Val Lys Leu Ser Ser  
 770 775 780  
 Gln Gln Ala  
 785

<210> 32  
 <211> 781  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human activity dependent neurotrophic factor III  
 (ADNF III)

<400> 32  
 Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val  
 1 5 10 15  
 Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly  
 20 25 30  
 Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu  
 35 40 45  
 Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg  
 50 55 60  
 Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser  
 65 70 75 80  
 Leu Ser Ser Gly His Leu Lys Ser Pro Ser Leu Ser His Ser Gln Ala  
 85 90 95

Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr  
 100 105 110  
 Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys  
 115 120 125  
 Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe  
 130 135 140  
 Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile  
 145 150 155 160  
 Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr  
 165 170 175  
 Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser  
 180 185 190  
 Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala  
 195 200 205  
 His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp  
 210 215 220  
 Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn  
 225 230 235 240  
 Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu  
 245 250 255  
 Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro  
 260 265 270  
 Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro  
 275 280 285  
 Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro  
 290 295 300  
 Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His  
 305 310 315 320  
 His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu  
 325 330 335  
 Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser  
 340 345 350  
 Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly  
 355 360 365  
 Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg  
 370 375 380  
 Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln  
 385 390 395 400  
 Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp  
 405 410 415



Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala  
 420 425 430  
 Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser  
 435 440 445  
 Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu  
 450 455 460  
 Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala  
 465 470 475 480  
 Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys  
 485 490 495  
 Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys  
 500 505 510  
 Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His  
 515 520 525  
 Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys  
 530 535 540  
 Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn  
 545 550 555 560  
 Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe  
 565 570 575  
 Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu  
 580 585 590  
 Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln  
 595 600 605  
 Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro  
 610 615 620  
 Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp  
 625 630 635 640  
 Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly  
 645 650 655  
 Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro  
 660 665 670  
 Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser  
 675 680 685  
 Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln  
 690 695 700  
 Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser  
 705 710 715 720  
 Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu  
 725 730 735

Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp  
                   740                  745                  750

Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Thr Glu Pro Met His  
                   755                  760                  765

Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala  
                   770                  775                  780

<210> 33  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:ADNF III  
           polypeptide

<400> 33  
 Gly Gly Asn Ala Pro Val Ser Ile Pro Gln  
       1                  5                  10

<210> 34  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:ADNF III  
           polypeptide

<400> 34  
 Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser  
       1                  5                  10

<210> 35  
 <211> 15  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:ADNF III  
           polypeptide

<400> 35  
 Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser  
       1                  5                  10                  15

<210> 36  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:ADNF-9 active  
           peptide adsorbed onto bovine serum albumin (BSA)  
           as antigen

<400> 36

Ser Ala Leu Leu Arg Ser Ile Pro Ala  
1 5

<210> 37

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:ADNF  
I/PIF1-related sequence

<400> 37

Ile Gln Leu Glu Thr Glu Ile Gln Glu Lys Gln Ile Ile  
1 5 10

<210> 38

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:cyclophilin  
mRNA mimic primer

<400> 38

atggcacagg aggaaagagc aatgcaggca aagacacc

38

<210> 39

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:neuropeptide  
cleavage site

<400> 39

Lys Lys Arg Lys  
1

<210> 40

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:neuropeptide  
cleavage site

<400> 40

Lys Arg Lys Lys  
1

<210> 41  
 <211> 800  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(800)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 41  
 Met Val Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly  
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 Val Asn Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val  
                   20                  25                  30  
 Lys Ser Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly  
                   35                  40                  45  
 Leu Gly Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val  
                   50                  55                  60  
 Lys Gln Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser  
                   65                  70                  75                  80  
 Glu Gln Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn  
                   85                  90                  95  
 Ala Ser Ser Leu Ser Ser Gly His Leu Lys Ser Pro Ser Leu Ser His  
                   100                  105                  110  
 Ser Gln Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala  
                   115                  120                  125  
 Ala Ala Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp  
                   130                  135                  140  
 Lys Ile Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser  
                   145                  150                  155                  160  
 Val His Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala  
                   165                  170                  175  
 Asn Tyr Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys  
                   180                  185                  190  
 Asn Arg Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His  
                   195                  200                  205  
 Gly Leu Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys  
                   210                  215                  220  
 Met Ala Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro  
                   225                  230                  235                  240  
 Lys Thr Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser  
                   245                  250                  255  
 His Thr Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala  
                   260                  265                  270

Pro Ala Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro  
 275 280 285  
 Pro Lys Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys  
 290 295 300  
 Ser Ser Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr  
 305 310 315 320  
 Leu Cys Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala  
 325 330 335  
 Leu Ala His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His  
 340 345 350  
 Pro Val Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val  
 355 360 365  
 Tyr Thr Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His  
 370 375 380  
 Cys Arg Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala  
 385 390 395 400  
 Pro Ser Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr  
 405 410 415  
 Tyr Glu Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp  
 420 425 430  
 Asp Ser Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val  
 435 440 445  
 Val Leu Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala  
 450 455 460  
 Arg Lys Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr  
 465 470 475 480  
 Arg Arg Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser  
 485 490 495  
 Asp Ile Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp  
 500 505 510  
 Cys Glu Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu  
 515 520 525  
 Leu Asn Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe  
 530 535 540  
 Glu Asn His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala  
 545 550 555 560  
 Asp Lys Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser  
 565 570 575  
 Phe Glu Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp  
 580 585 590

Pro Val Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu  
 595 600 605  
 His Val Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys  
 610 615 620  
 Leu Asp Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr  
 625 630 635 640  
 Glu Glu Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp  
 645 650 655  
 Gln Asp Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser  
 660 665 670  
 Gly Pro Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu  
 675 680 685  
 Met Lys Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala  
 690 695 700  
 Arg Ser Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp  
 705 710 715 720  
 Arg Glu Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly  
 725 730 735  
 Phe Trp Ser Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp  
 740 745 750  
 Glu Arg Leu Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp  
 755 760 765  
 Ser Glu Asp Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Thr Glu  
 770 775 780  
 Pro Met His Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala  
 785 790 795 800

<210> 42

<211> 15

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(15)

<223> translation of H3' human ADNF III cDNA clone

<400> 42

Val Pro Gly Ser Leu Ala Leu Val Thr Cys Cys Ser Leu Glu Leu  
 1 5 10 15

<210> 43  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 43  
 Leu Gln Ser Cys Leu Leu Thr Gly Thr Ala Leu  
 1 5 10

<210> 44  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(20)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 44  
 Val Leu Val Gly Leu Trp Gly Met Trp Pro Leu Gln Phe Gln Trp Leu  
 1 5 10 15

Phe Leu Ser Leu  
 20

<210> 45  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(11)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 45  
 Gln Asp Arg Leu Phe Leu Leu Gln Asn Leu Leu  
 1 5 10

<210> 46  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(6)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 46  
 Leu Asn Val Lys Asn Gln  
 1 5

<210> 47  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(4)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 47  
 Ala Gly Asp Ser  
 1

<210> 48  
 <211> 39  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(39)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 48  
 Ile Leu Thr Arg Lys Ser Arg Gly Leu Phe Leu Ser Ala Phe Ser Thr  
 1 5 10 15  
 Phe Leu Ser Leu Cys Glu Met Ile Gly Gln Met Ser Leu Arg Ser Val  
 20 25 30  
 Lys Leu Ile His Met Val Val  
 35

<210> 49  
 <211> 25  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 49  
 Gly Gln His Thr Ser Tyr Gln Ser Asn Val Tyr Ser Arg Leu Trp Glu  
 1 5 10 15  
 Lys Arg Phe Phe Phe Met Tyr Ser Phe  
 20 25

<210> 50  
 <211> 10  
 <212> PRT  
 <213> Homo sapiens



<220>  
 <221> PEPTIDE  
 <222> (1)..(10)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 50  
 Ile Val Glu Met Tyr Ile Cys Thr Val Phe  
 1 5 10

<210> 51  
 <211> 4  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(4)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 51  
 Thr Tyr Ser Lys  
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<210> 52  
 <211> 12  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(12)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 52  
 Ser Cys Tyr Cys Val Pro Ile Ile Asp Phe Phe Phe  
 1 5 10

<210> 53  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(20)  
 <223> translation of H3' human ADNF III cDNA clone

<400> 53  
 Cys Cys Pro Cys Cys Val Ile Asn Ala Leu Ser Ser Leu Pro Ser Lys  
 1 5 10 15

Ser Ser Lys Leu  
 20

<210> 54  
 <211> 2487  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)..(2487)  
 <223> an additional mouse activity dependent  
 neurotrophic factor III (ADNF III) cDNA clone

<400> 54  
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 Met Gly Leu Pro Pro Arg Ile Ser Ser Leu Ala Ser Gly Asn Val Arg  
 1 5 10 15

tcg ttg cca tca cag cag atg gta aac cga ttg tca ata cca aag ccc 96  
 Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser Ile Pro Lys Pro  
 20 25 30

aac tta aat tca acg gga gtc aac atg atg tcc aat gtt cac ctg cag 144  
 Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Asn Val His Leu Gln  
 35 40 45

caa aac aac tat gga gtc aaa tct gtg ggc cag agc tat ggt gtt ggc 192  
 Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Ser Tyr Gly Val Gly  
 50 55 60

cag tca gtg agg ctg gga cta ggt ggc aat gct cca gtt tcc atc cct 240  
 Gln Ser Val Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro  
 65 70 75 80

caa cag tct cag tcc gtg aaa cag tta ctt cca agt ggg aat ggg agg 288  
 Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser Gly Asn Gly Arg  
 85 90 95

tct ttt ggg cta ggt gct gag cag agg ccc cca gca gca gcc agg tac 336  
 Ser Phe Gly Leu Gly Ala Glu Gln Arg Pro Pro Ala Ala Ala Arg Tyr  
 100 105 110

tcc ctg cag act gcc aac acc tct cta ccc cca ggc caa gtg aag tct 384  
 Ser Leu Gln Thr Ala Asn Thr Ser Leu Pro Pro Gly Gln Val Lys Ser  
 115 120 125

ccc tct gtg tct cag tca cag gca tct aga gta tta ggt cag tcc agt 432  
 Pro Ser Val Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln Ser Ser  
 130 135 140

tct aaa cct cca cca gcc gcc aca ggc cct cct cca agc aac cac tgt 480  
 Ser Lys Pro Pro Pro Ala Ala Thr Gly Pro Pro Pro Ser Asn His Cys  
 145 150 155 160

gcc act cag aag tgg aaa atc tgt aca atc tgt aac gag ctt ttc cct 528  
 Ala Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu Phe Pro  
 165 170 175

gag aat gtc tat agc gtt cac ttc gaa aag gag cat aaa gct gag aaa 576  
 Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala Glu Lys  
 180 185 190

gtc cca gcc gta gct aac tac att atg aaa ata cac aat ttt act agc	624
Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe Thr Ser	
195 200 205	
aaa tgc ctc tac tgt aat cgc tat ttg cct aca gat acc cta ctc aac	672
Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu Leu Asn	
210 215 220	
cat atg tta att cat ggt ctg tct tgt ccg tat tgc cgt tcc acc ttc	720
His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser Thr Phe	
225 230 235 240	
aat gat gta gag aag atg gca gca cac atg cga atg gtt cat att gat	768
Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His Ile Asp	
245 250 255	
gaa gag atg ggg cct aaa acg gat tct act ttg agc ttt gat ttg aca	816
Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp Leu Thr	
260 265 270	
ttg caa cag ggc agt cac acc aac att cat ctc ctg gtg acc aca tac	864
Leu Gln Gln Gly Ser His Thr Asn Ile His Leu Leu Val Thr Thr Tyr	
275 280 285	
aac ctg agg gat gcc ccg gct gaa tca gtt gct tac cat gcc caa aat	912
Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala Tyr His Ala Gln Asn	
290 295 300	
aat gcc cca gtt cct cca aag cca caa cca aaa gtt cag gaa aaa gca	960
Asn Ala Pro Val Pro Pro Lys Pro Gln Pro Lys Val Gln Glu Lys Ala	
305 310 315 320	
gat gtc ccg gtt aaa agt tca cct caa gct gca gtg ccc tat aaa aaa	1008
Asp Val Pro Val Lys Ser Ser Pro Gln Ala Ala Val Pro Tyr Lys Lys	
325 330 335	
gat gtt ggg aag acc ctt tgc cct ctt tgc ttt tca ata cta aaa gga	1056
Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu Lys Gly	
340 345 350	
ccc ata tct gat gca ctt gca cat cat tta cga gaa aga cac caa gtt	1104
Pro Ile Ser Asp Ala Leu Ala His His Leu Arg Glu Arg His Gln Val	
355 360 365	
att cag aca gtt cat ccg gtt gag aaa aag cta act tac aaa tgt atc	1152
Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys Cys Ile	
370 375 380	
cat tgc ctt ggt gtg tat act agc aac atg aca gcc tca acc atc act	1200
His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr Ala Ser Thr Ile Thr	
385 390 395 400	
ctg cat cta gtc cac tgc agg ggt gtt gga aaa acc cag aat ggc cag	1248
Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn Gly Gln	
405 410 415	
gac aag aca aac gca cct tct cgg ctc aat cag tct cca ggc ctg gcc	1296
Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Gly Leu Ala	
420 425 430	

cct	gtg	aag	cgc	acg	tat	gag	cag	atg	gag	ttt	cca	ctg	cta	aaa	aag	1344
Pro	Val	Lys	Arg	Thr	Tyr	Glu	Gln	Met	Glu	Phe	Pro	Leu	Leu	Lys	Lys	
		435					440					445				
cgg	aag	ctg	gag	gag	gat	gct	gat	tcc	cct	agc	tgc	ttt	gaa	gag	aag	1392
Arg	Lys	Leu	Glu	Glu	Asp	Ala	Asp	Ser	Pro	Ser	Cys	Phe	Glu	Glu	Lys	
	450					455					460					
cca	gaa	gag	cct	gtt	gtt	tta	gct	tta	gac	ccc	aag	ggt	cat	gaa	gat	1440
Pro	Glu	Glu	Pro	Val	Val	Leu	Ala	Leu	Asp	Pro	Lys	Gly	His	Glu	Asp	
465					470					475					480	
gat	tct	tat	gag	gct	agg	aaa	agc	ttt	ctc	aca	aag	tac	ttc	aac	aaa	1488
Asp	Ser	Tyr	Glu	Ala	Arg	Lys	Ser	Phe	Leu	Thr	Lys	Tyr	Phe	Asn	Lys	
			485						490					495		
cag	ccc	tat	ccc	acc	agg	aga	gaa	att	gag	aag	tta	gct	gcc	agt	cta	1536
Gln	Pro	Tyr	Pro	Thr	Arg	Arg	Glu	Ile	Glu	Lys	Leu	Ala	Ala	Ser	Leu	
		500					505					510				
tgg	cta	tgg	aag	agt	gac	att	gcc	tcc	cat	ttc	agt	aac	aag	agg	aag	1584
Trp	Leu	Trp	Lys	Ser	Asp	Ile	Ala	Ser	His	Phe	Ser	Asn	Lys	Arg	Lys	
	515					520						525				
aag	tgt	gtc	cgc	gac	tgt	gaa	aag	tac	aag	cct	ggt	gtg	ctg	cta	ggt	1632
Lys	Cys	Val	Arg	Asp	Cys	Glu	Lys	Tyr	Lys	Pro	Gly	Val	Leu	Leu	Gly	
	530					535					540					
ttt	aac	atg	aaa	gaa	tta	aat	aaa	gtc	aaa	cac	gag	atg	gat	ttt	gat	1680
Phe	Asn	Met	Lys	Glu	Leu	Asn	Lys	Val	Lys	His	Glu	Met	Asp	Phe	Asp	
545					550					555					560	
gct	gag	tgg	ctg	ttt	gaa	aat	cac	gat	gag	aaa	gac	tca	aga	gtc	aat	1728
Ala	Glu	Trp	Leu	Phe	Glu	Asn	His	Asp	Glu	Lys	Asp	Ser	Arg	Val	Asn	
			565					570						575		
gct	agc	aag	act	gtt	gac	aaa	aag	cat	aac	ctt	ggg	aaa	gaa	gat	gat	1776
Ala	Ser	Lys	Thr	Val	Asp	Lys	Lys	His	Asn	Leu	Gly	Lys	Glu	Asp	Asp	
			580					585					590			
agc	ttc	tca	gat	agt	ttt	gaa	cat	ttg	gaa	gaa	gaa	tcc	aat	gga	agc	1824
Ser	Phe	Ser	Asp	Ser	Phe	Glu	His	Leu	Glu	Glu	Glu	Ser	Asn	Gly	Ser	
		595				600						605				
ggg	agt	cct	ttt	gac	cct	gtc	ttt	gaa	gtt	gag	cct	aaa	att	ccc	agt	1872
Gly	Ser	Pro	Phe	Asp	Pro	Val	Phe	Glu	Val	Glu	Pro	Lys	Ile	Pro	Ser	
	610					615					620					
gat	aat	tta	gag	gag	cct	gta	ccg	aag	gtt	att	ccg	gaa	ggt	gct	ttg	1920
Asp	Asn	Leu	Glu	Glu	Pro	Val	Pro	Lys	Val	Ile	Pro	Glu	Gly	Ala	Leu	
625					630					635					640	
gaa	tct	gag	aag	cta	gac	caa	aaa	gag	gag	gag	gag	gag	gag	gag	gag	1968
Glu	Ser	Glu	Lys	Leu	Asp	Gln	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
			645					650						655		
gag	gat	ggt	tca	aaa	tat	gaa	act	atc	cat	ttg	act	gag	gaa	cca	gcc	2016
Glu	Asp	Gly	Ser	Lys	Tyr	Glu	Thr	Ile	His	Leu	Thr	Glu	Glu	Pro	Ala	
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<400> 55
Met Gly Leu Pro Pro Arg Ile Ser Ser Leu Ala Ser Gly Asn Val Arg
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Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser Ile Pro Lys Pro
      20             25             30

Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Asn Val His Leu Gln
      35             40             45

Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Ser Tyr Gly Val Gly
      50             55             60

Gln Ser Val Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile Pro
      65             70             75             80

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Gln	Gln	Ser	Gln	Ser	Val	Lys	Gln	Leu	Leu	Pro	Ser	Gly	Asn	Gly	Arg		
				85						90						95	
Ser	Phe	Gly	Leu	Gly	Ala	Glu	Gln	Arg	Pro	Pro	Ala	Ala	Ala	Arg	Tyr		
			100						105							110	
Ser	Leu	Gln	Thr	Ala	Asn	Thr	Ser	Leu	Pro	Pro	Gly	Gln	Val	Lys	Ser		
		115						120									
Pro	Ser	Val	Ser	Gln	Ser	Gln	Ala	Ser	Arg	Val	Leu	Gly	Gln	Ser	Ser		
		130						135								140	
Ser	Lys	Pro	Pro	Pro	Ala	Ala	Thr	Gly	Pro	Pro	Pro	Ser	Asn	His	Cys		
				145		150										160	
Ala	Thr	Gln	Lys	Trp	Lys	Ile	Cys	Thr	Ile	Cys	Asn	Glu	Leu	Phe	Pro		
				165						170						175	
Glu	Asn	Val	Tyr	Ser	Val	His	Phe	Glu	Lys	Glu	His	Lys	Ala	Glu	Lys		
			180						185							190	
Val	Pro	Ala	Val	Ala	Asn	Tyr	Ile	Met	Lys	Ile	His	Asn	Phe	Thr	Ser		
		195						200									
Lys	Cys	Leu	Tyr	Cys	Asn	Arg	Tyr	Leu	Pro	Thr	Asp	Thr	Leu	Leu	Asn		
		210						215								220	
His	Met	Leu	Ile	His	Gly	Leu	Ser	Cys	Pro	Tyr	Cys	Arg	Ser	Thr	Phe		
				225		230										240	
Asn	Asp	Val	Glu	Lys	Met	Ala	Ala	His	Met	Arg	Met	Val	His	Ile	Asp		
			245						250							255	
Glu	Glu	Met	Gly	Pro	Lys	Thr	Asp	Ser	Thr	Leu	Ser	Phe	Asp	Leu	Thr		
		260						265								270	
Leu	Gln	Gln	Gly	Ser	His	Thr	Asn	Ile	His	Leu	Leu	Val	Thr	Thr	Tyr		
		275						280								285	
Asn	Leu	Arg	Asp	Ala	Pro	Ala	Glu	Ser	Val	Ala	Tyr	His	Ala	Gln	Asn		
		290						295								300	
Asn	Ala	Pro	Val	Pro	Pro	Lys	Pro	Gln	Pro	Lys	Val	Gln	Glu	Lys	Ala		
				305		310										320	
Asp	Val	Pro	Val	Lys	Ser	Ser	Pro	Gln	Ala	Ala	Val	Pro	Tyr	Lys	Lys		
			325						330							335	
Asp	Val	Gly	Lys	Thr	Leu	Cys	Pro	Leu	Cys	Phe	Ser	Ile	Leu	Lys	Gly		
		340						345								350	
Pro	Ile	Ser	Asp	Ala	Leu	Ala	His	His	Leu	Arg	Glu	Arg	His	Gln	Val		
		355						360								365	
Ile	Gln	Thr	Val	His	Pro	Val	Glu	Lys	Lys	Leu	Thr	Tyr	Lys	Cys	Ile		
		370						375								380	
His	Cys	Leu	Gly	Val	Tyr	Thr	Ser	Asn	Met	Thr	Ala	Ser	Thr	Ile	Thr		
				385		390										400	

Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn Gly Gln  
 405 410 415  
 Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Gly Leu Ala  
 420 425 430  
 Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe Pro Leu Leu Lys Lys  
 435 440 445  
 Arg Lys Leu Glu Glu Asp Ala Asp Ser Pro Ser Cys Phe Glu Glu Lys  
 450 455 460  
 Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro Lys Gly His Glu Asp  
 465 470 475 480  
 Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe Asn Lys  
 485 490 495  
 Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala Ser Leu  
 500 505 510  
 Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys Arg Lys  
 515 520 525  
 Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu Leu Gly  
 530 535 540  
 Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp Phe Asp  
 545 550 555 560  
 Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg Val Asn  
 565 570 575  
 Ala Ser Lys Thr Val Asp Lys Lys His Asn Leu Gly Lys Glu Asp Asp  
 580 585 590  
 Ser Phe Ser Asp Ser Phe Glu His Leu Glu Glu Glu Ser Asn Gly Ser  
 595 600 605  
 Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu Pro Lys Ile Pro Ser  
 610 615 620  
 Asp Asn Leu Glu Glu Pro Val Pro Lys Val Ile Pro Glu Gly Ala Leu  
 625 630 635 640  
 Glu Ser Glu Lys Leu Asp Gln Lys Glu Glu Glu Glu Glu Glu Glu  
 645 650 655  
 Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Ala  
 660 665 670  
 Lys Leu Met His Asp Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val  
 675 680 685  
 Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser  
 690 695 700  
 Gln Gln Ile Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly  
 705 710 715 720

Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys  
                     725                    730                    735  
 Pro Ala Ala Lys Lys Lys Ala Thr Val Gln Asp Asp Thr Glu Gln Leu  
                     740                    745                    750  
 Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser Lys  
                     755                    760                    765  
 Asp Gln Ser Gln Trp Glu Asn Ala Ser Glu Asn Ala Glu Arg Leu Pro  
                     770                    775                    780  
 Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp Gly  
 785                    790                    795                    800  
 Glu His Phe Asp Ser Met Thr Asp Gly Val Ala Asp Pro Met His Gly  
                     805                    810                    815  
 Ser Leu Thr Gly Val Lys Leu Ser Ser Gln Gln Ala  
                     820                    825

<210> 56

<211> 2181

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(2181)

<223> H3 human activity dependent neurotrophic factor  
 III (ADNF III) clone

<400> 56

cgg tct tta cca tca cag cag atg gtg aat cga ctc tca ata cca aag 48  
 Arg Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser Ile Pro Lys  
   1                    5                    10                    15

cct aac tta aat tct aca gga gtc aac atg atg tcc agt gtt cat ctg 96  
 Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Ser Val His Leu  
                     20                    25                    30

cag cag aac aac tat gga gtc aaa tct gta ggc cag ggt tac agt gtt 144  
 Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Gly Tyr Ser Val  
                     35                    40                    45

ggt cag tca atg aga ctg ggt cta ggt ggc aac gca cca gtt tcc att 192  
 Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile  
                     50                    55                    60

cct caa caa tct cag tct gta aag cag tta ctt cca agt gga aac gga 240  
 Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser Gly Asn Gly  
   65                    70                    75                    80

agg tct tat ggg ctt ggg tca gag cag agg tcc cag gca cca gca aga 288  
 Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala Pro Ala Arg  
                     85                    90                    95

tac tcc ctg cag tct gct aat gcc tct tct ctc tca tcg ggc cag tta 336  
 Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu Ser Ser Gly Gln Leu  
                     100                    105                    110



aag tct cct tcc ctc tct cag tca cag gca tcc aga gtg tta ggt cag	384
Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln	
115 120 125	
tcc agt tcc aaa cct gct gca gct gcc aca ggc cct ccc cca ggt aac	432
Ser Ser Ser Lys Pro Ala Ala Ala Thr Gly Pro Pro Pro Gly Asn	
130 135 140	
act tcc tca act caa aag tgg aaa ata tgt aca atc tgt aat gag ctt	480
Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu	
145 150 155 160	
ttt cct gaa aat gtc tat agt gtg cac ttc gaa aaa gaa cat aaa gct	528
Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala	
165 170 175	
gag aaa gtc cca gca gta gcc aac tac att atg aaa ata cac aat ttt	576
Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe	
180 185 190	
act agc aaa tgc ctc tac tgt aat cgc tat tta ccc aca gat act ctg	624
Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu	
195 200 205	
ctc aac cat atg tta att cat ggt ctg tct tgt cca tat tgc cgt tca	672
Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser	
210 215 220	
act ttc aat gat gtg gaa aag atg gcc gca cac atg cgg atg gtt cac	720
Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His	
225 230 235 240	
att gat gaa gag atg gga cct aaa aca gat tct act ttg agt ttt gat	768
Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp	
245 250 255	
ttg aca ttg cag cag ggt agt cac act aac atc cat ctc ctg gta act	816
Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile His Leu Leu Val Thr	
260 265 270	
aca tac aat ctg agg gat gcc cca gct gaa tct gtt gct tac cat gcc	864
Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala Tyr His Ala	
275 280 285	
caa aat aat cct cca gtt cct cca aag cca cag cca aag gtt cag gaa	912
Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln Pro Lys Val Gln Glu	
290 295 300	
aag gca gat atc cct gta aaa agt tca cct caa gct gca gtg ccc tat	960
Lys Ala Asp Ile Pro Val Lys Ser Ser Pro Gln Ala Ala Val Pro Tyr	
305 310 315 320	
aaa aaa gat gtt ggg aaa acc ctt tgt cct ctt tgc ttt tca atc cta	1008
Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu	
325 330 335	
aaa gga ccc ata tct gat gca ctt gca cat cac tta cga gag agg cac	1056
Lys Gly Pro Ile Ser Asp Ala Leu Ala His His Leu Arg Glu Arg His	
340 345 350	

caa gtt att cag acg gtt cat cca gtt gag aaa aag ctc acc tac aaa	1104
Gln Val Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys	
355 360 365	
tgt atc cat tgc ctt ggt gtg tat acc agc aac atg acc gcc tca act	1152
Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr Ala Ser Thr	
370 375 380	
atc act ctg cat cta gtt cac tgc agg ggc gtt gga aag acc caa aat	1200
Ile Thr Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn	
385 390 395 400	
ggc cag gat aag aca aat gca ccc tct cgg ctt aat cag tct cca agt	1248
Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Ser	
405 410 415	
ctg gca cct gtg aag cgc act tac gag caa atg gaa ttt ccc tta ctg	1296
Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe Pro Leu Leu	
420 425 430	
aaa aaa cga aag tta gat gat gat agt gat tca ccc agc ttc ttt gaa	1344
Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser Pro Ser Phe Phe Glu	
435 440 445	
gag aag cct gaa gag cct gtt gtt tta gct tta gac ccc aag ggt cat	1392
Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro Lys Gly His	
450 455 460	
gaa gat gat tcc tat gaa gcc agg aaa agc ttt cta aca aag tat ttc	1440
Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe	
465 470 475 480	
aac aaa cag ccc tat ccc acc agg aga gaa att gag aag cta gca gcc	1488
Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala	
485 490 495	
agt tta tgg tta tgg aag agt gac atc gct tcc cat ttt agt aac aaa	1536
Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys	
500 505 510	
agg aag aag tgt gtc cgt gat tgt gaa aag tac aag cct ggc gtg ttg	1584
Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu	
515 520 525	
ctg ggg ttt aac atg aaa gaa tta aat aaa gtc aag cat gag atg gat	1632
Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp	
530 535 540	
ttt gat gct gag tgg cta ttt gaa aat cat gat gag aag gat tcc aga	1680
Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg	
545 550 555 560	
gtc aat gct agt aag act gct gac aaa aag ctc aac ctt ggg aag gaa	1728
Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu Gly Lys Glu	
565 570 575	
gat gac agt tcc tca gac agt ttt gaa aat ttg gaa gaa gaa tcc aat	1776
Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu Glu Ser Asn	
580 585 590	

gaa agt ggt agc cct ttt gac cct gtt ttt gaa gtt gaa cct aaa atc 1824  
 Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu Pro Lys Ile  
 595 600 605  
  
 tct aac gat aac cca gag gaa cat gta ctg aag gta att cct gag gat 1872  
 Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val Ile Pro Glu Asp  
 610 615 620  
  
 gct tca gaa tct gag gag aag cta gac caa aaa gag gat ggt tca aaa 1920  
 Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp Gly Ser Lys  
 625 630 635 640  
  
 tac gaa act att cat ttg act gag gaa cca acc aaa cta atg cac aat 1968  
 Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu Met His Asn  
 645 650 655  
  
 gca tct gat agt gag gtt gac caa gac gat gtt gtt gag tgg aaa gac 2016  
 Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp  
 660 665 670  
  
 ggt gct tct cca tct gag agt ggg cct gga tcc caa caa gtg tca gac 2064  
 Gly Ala Ser Pro Ser Glu Ser Gly Gly Ser Gln Gln Val Ser Asp  
 675 680 685  
  
 ttt gag gac aat acc tgc gaa atg aaa cca gga acc tgg tct gac gag 2112  
 Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu  
 690 695 700  
  
 tct tcc caa agc gaa gat gca agg agc agt aag cca gct gcc aaa aaa 2160  
 Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys  
 705 710 715 720  
  
 aaa ggc tac cat gca agg tga 2181  
 Lys Gly Tyr His Ala Arg  
 725

&lt;210&gt; 57

&lt;211&gt; 726

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 57

Arg Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser Ile Pro Lys  
 1 5 10 15

Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Ser Val His Leu  
 20 25 30

Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Gly Tyr Ser Val  
 35 40 45

Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro Val Ser Ile  
 50 55 60

Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser Gly Asn Gly  
 65 70 75 80

Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala Pro Ala Arg  
 85 90 95

Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu Ser Ser Gly Gln Leu  
 100 105 110  
 Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val Leu Gly Gln  
 115 120 125  
 Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr Gly Pro Pro Pro Gly Asn  
 130 135 140  
 Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys Asn Glu Leu  
 145 150 155 160  
 Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu His Lys Ala  
 165 170 175  
 Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile His Asn Phe  
 180 185 190  
 Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr Asp Thr Leu  
 195 200 205  
 Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr Cys Arg Ser  
 210 215 220  
 Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg Met Val His  
 225 230 235 240  
 Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu Ser Phe Asp  
 245 250 255  
 Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile His Leu Leu Val Thr  
 260 265 270  
 Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala Tyr His Ala  
 275 280 285  
 Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln Pro Lys Val Gln Glu  
 290 295 300  
 Lys Ala Asp Ile Pro Val Lys Ser Ser Pro Gln Ala Ala Val Pro Tyr  
 305 310 315 320  
 Lys Lys Asp Val Gly Lys Thr Leu Cys Pro Leu Cys Phe Ser Ile Leu  
 325 330 335  
 Lys Gly Pro Ile Ser Asp Ala Leu Ala His His Leu Arg Glu Arg His  
 340 345 350  
 Gln Val Ile Gln Thr Val His Pro Val Glu Lys Lys Leu Thr Tyr Lys  
 355 360 365  
 Cys Ile His Cys Leu Gly Val Tyr Thr Ser Asn Met Thr Ala Ser Thr  
 370 375 380  
 Ile Thr Leu His Leu Val His Cys Arg Gly Val Gly Lys Thr Gln Asn  
 385 390 395 400  
 Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg Leu Asn Gln Ser Pro Ser  
 405 410 415

Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln Met Glu Phe Pro Leu Leu  
 420 425 430  
 Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp Ser Pro Ser Phe Phe Glu  
 435 440 445  
 Glu Lys Pro Glu Glu Pro Val Val Leu Ala Leu Asp Pro Lys Gly His  
 450 455 460  
 Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser Phe Leu Thr Lys Tyr Phe  
 465 470 475 480  
 Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu Ile Glu Lys Leu Ala Ala  
 485 490 495  
 Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala Ser His Phe Ser Asn Lys  
 500 505 510  
 Arg Lys Lys Cys Val Arg Asp Cys Glu Lys Tyr Lys Pro Gly Val Leu  
 515 520 525  
 Leu Gly Phe Asn Met Lys Glu Leu Asn Lys Val Lys His Glu Met Asp  
 530 535 540  
 Phe Asp Ala Glu Trp Leu Phe Glu Asn His Asp Glu Lys Asp Ser Arg  
 545 550 555 560  
 Val Asn Ala Ser Lys Thr Ala Asp Lys Lys Leu Asn Leu Gly Lys Glu  
 565 570 575  
 Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn Leu Glu Glu Glu Ser Asn  
 580 585 590  
 Glu Ser Gly Ser Pro Phe Asp Pro Val Phe Glu Val Glu Pro Lys Ile  
 595 600 605  
 Ser Asn Asp Asn Pro Glu Glu His Val Leu Lys Val Ile Pro Glu Asp  
 610 615 620  
 Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp Gly Ser Lys  
 625 630 635 640  
 Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu Met His Asn  
 645 650 655  
 Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu Trp Lys Asp  
 660 665 670  
 Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser Gln Gln Val Ser Asp  
 675 680 685  
 Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp Ser Asp Glu  
 690 695 700  
 Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys Pro Ala Ala Lys Lys  
 705 710 715 720  
 Lys Gly Tyr His Ala Arg  
 725

<210> 58  
 <211> 4193  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (492)..(3116)  
 <223> H7 human activity dependent neurotrophic factor  
 III (ADNF III) clone

<400> 58  
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 tcttctctgc ctacaaaagt catttccgca atgtccatag tgaagacttt gaaaatagga 120  
 ttctccttaa ttgcccctac tgtaccttca atgcagacaa aaagactttg gaaacacaca 180  
 ttaaaatatt tcatgctccg aacgccagcg caccaagtag cagcttcagc actttcaaag 240  
 ataaaaccaa aaatgatggc cttaaactta agcaggctga cagtgtagag caagctgttt 300  
 attactgtaa gaagtgcact taccgagatc ctctttatga aatagttagg aagcacattt 360  
 acagggaaca ttttcagcat gtggcagcac cttacatagc aaaggcagga gaaaaatcac 420  
 tcaatggggc agtcccctta ggctcgaatg cccgagaaga gagtagtatt cactgcaagc 480  
 gatgcctttt c atg cca aag tcc tat gaa gct ttg gta cag cat gtc atc 530  
 Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val Ile  
 1 5 10  
 gaa gac cat gaa cgt ata ggc tat cag gtc act gcc atg att ggg cac 578  
 Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly His  
 15 20 25  
 aca aat gta gtg gtt ccc cga tcc aaa ccc ttg atg cta att gct ccc 626  
 Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala Pro  
 30 35 40 45  
 aaa cct caa gac aag aag agc atg gga ctc cca cca agg atc ggt tcc 674  
 Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly Ser  
 50 55 60  
 ctt gct tct gga aat gtc cgg tct tta cca tca cag cag atg gtg aat 722  
 Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val Asn  
 65 70 75  
 cga ctc tca ata cca aag cct aac tta aat tct aca gga gtc aac atg 770  
 Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn Met  
 80 85 90  
 atg tcc agt gtt cat ctg cag cag aac aac tat gga gtc aaa tct gta 818  
 Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val  
 95 100 105  
 ggc cag ggt tac agt gtt ggt cag tca atg aga ctg ggt cta ggt ggc 866  
 Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly  
 110 115 120 125

aac gca cca gtt tcc att cct caa caa tct cag tct gta aag cag tta	914
Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu	
130 135 140	
ctt cca agt gga aac gga agg tct tat ggg ctt ggg tca gag cag agg	962
Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg	
145 150 155	
tcc cag gca cca gca aga tac tcc ctg cag tct gct aat gcc tct tct	1010
Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser	
160 165 170	
ctc tca tcg ggc cag tta aag tct cct tcc ctc tct cag tca cag gca	1058
Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala	
175 180 185	
tcc aga gtg tta ggt cag tcc agt tcc aaa cct gct gca gct gcc aca	1106
Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Thr	
190 195 200 205	
ggc cct ccc cca ggt aac act tcc tca act caa aag tgg aaa ata tgt	1154
Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys	
210 215 220	
aca atc tgt aat gag ctt ttt cct gaa aat gtc tat agt gtg cac ttc	1202
Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe	
225 230 235	
gaa aaa gaa cat aaa gct gag aaa gtc cca gca gta gcc aac tac att	1250
Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile	
240 245 250	
atg aaa ata cac aat ttt act agc aaa tgc ctc tac tgt aat cgc tat	1298
Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr	
255 260 265	
tta ccc aca gat act ctg ctc aac cat atg tta att cat ggt ctg tct	1346
Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser	
270 275 280 285	
tgt cca tat tgc cgt tca act ttc aat gat gtg gaa aag atg gcc gca	1394
Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala	
290 295 300	
cac atg cgg atg gtt cac att gat gaa gag atg gga cct aaa aca gat	1442
His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp	
305 310 315	
tct act ttg agt ttt gat ttg aca ttg cag cag ggt agt cac act aac	1490
Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn	
320 325 330	
atc cat ctc ctg gta act aca tac aat ctg agg gat gcc cca gct gaa	1538
Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu	
335 340 345	
tct gtt gct tac cat gcc caa aat aat cct cca gtt cct cca aag cca	1586
Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro	
350 355 360 365	

cag cca aag gtt cag gaa aag gca gat atc cct gta aaa agt tca cct	1634
Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser Pro	
370 375 380	
caa gct gca gtg ccc tat aaa aaa gat gtt ggg aaa acc ctt tgt cct	1682
Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys Pro	
385 390 395	
ctt tgc ttt tca atc cta aaa gga ccc ata tct gat gca ctt gca cat	1730
Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala His	
400 405 410	
cac tta cga gag agg cac caa gtt att cag acg gtt cat cca gtt gag	1778
His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val Glu	
415 420 425	
aaa aag ctc acc tac aaa tgt atc cat tgc ctt ggt gtg tat acc agc	1826
Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr Ser	
430 435 440 445	
aac atg acc gcc tca act atc act ctg cat cta gtt cac tgc agg ggc	1874
Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg Gly	
450 455 460	
gtt gga aag acc caa aat ggc cag gat aag aca aat gca ccc tct cgg	1922
Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser Arg	
465 470 475	
ctt aat cag tct cca agt ctg gca cct gtg aag cgc act tac gag caa	1970
Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu Gln	
480 485 490	
atg gaa ttt ccc tta ctg aaa aaa cga aag tta gat gat gat agt gat	2018
Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser Asp	
495 500 505	
tca ccc agc ttc ttt gaa gag aag cct gaa gag cct gtt gtt tta gct	2066
Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu Ala	
510 515 520 525	
tta gac ccc aag ggt cat gaa gat gat tcc tat gaa gcc agg aaa agc	2114
Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys Ser	
530 535 540	
ttt cta aca aag tat ttc aac aaa cag ccc tat ccc acc agg aga gaa	2162
Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg Glu	
545 550 555	
att gag aag cta gca gcc agt tta tgg tta tgg aag agt gac atc gct	2210
Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile Ala	
560 565 570	
tcc cat ttt agt aac aaa agg aag aag tgt gtc cgt gat tgt gaa aag	2258
Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu Lys	
575 580 585	
tac aag cct ggc gtg ttg ctg ggg ttt aac atg aaa gaa tta aat aaa	2306
Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn Lys	
590 595 600 605	



gtc aag cat gag atg gat ttt gat gct gag tgg cta ttt gaa aat cat	2354
Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn His	
610 615 620	
gat gag aag gat tcc aga gtc aat gct agt aag act gct gac aaa aag	2402
Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys Lys	
625 630 635	
ctc aac ctt ggg aag gaa gat gac agt tcc tca gac agt ttt gaa aat	2450
Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu Asn	
640 645 650	
ttg gaa gaa gaa tcc aat gaa agt ggt agc cct ttt gac cct gtt ttt	2498
Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val Phe	
655 660 665	
gaa gtt gaa cct aaa atc tct aac gat aac cca gaa gaa cat gta ctg	2546
Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val Leu	
670 675 680 685	
aag gta att cct gag gat gct tca gaa tct gag gag aag cta gac caa	2594
Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln	
690 695 700	
aaa gaa gat ggt tca aaa tac gaa act att cat ttg act gag gaa cca	2642
Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro	
705 710 715	
acc aaa cta atg cac aat gca tct gat agt gag gtt gac caa gac gat	2690
Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp	
720 725 730	
gtt gtt gag tgg aaa gac ggt gct tct cca tct gag agt ggg cct gga	2738
Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly	
735 740 745	
tcc caa caa gtg tca gac ttt gag gac aat acc tgc gaa atg aaa cca	2786
Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro	
750 755 760 765	
gga acc tgg tct gac gag tct tcc caa agc gaa gat gca agg agc agt	2834
Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser	
770 775 780	
aag cca gct gcc aaa aaa aag gct acc atg caa ggt gac aga gag cag	2882
Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln	
785 790 795	
ttg aaa tgg aag aat agt tcc tat gga aaa gtt gaa ggg ttt tgg tct	2930
Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser	
800 805 810	
aag gac cag tca cag tgg aag aat gca tct gag aat gat gag cgc tta	2978
Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu	
815 820 825	
tct aac ccc cag att gag tgg cag aat agc aca att gac agt gag gat	3026
Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp	
830 835 840 845	

ggg gaa cag ttt gac aac atg act gat gga gta gct gag ccc atg cat 3074  
 Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met His  
                   850                  855                  860

ggc agc tta gcc gga gtt aaa ctg agc agc caa cag gcc taagtgccag 3123  
 Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala  
                   865                  870

gttccctggc attggtgaca tgctgcagcc tggaactctg atctccagtg tgactgcaaa 3183

gctgtcttct cactggtact gccttgtagg tactggttgg actgtggggc atgtggccgc 3243

tgcaagttcca gtggttattt ctaagtctat gacaggacag gctgttcttg cttcagaacc 3303

ttctctgaca gacacggtaa ctaaagtga aaaaccaata agctggtgac tcatgaatac 3363

acacgaggaa aagcagaggt ttattttatc tgccttttca acatttcttt ccctctgtga 3423

aatgattggt cagatgtctt tgagaagtgt taaactaatt cacatggtag tgtagggcca 3483

acatacaagc taccagtcta atgtgtatag tagactttgg gaaaagcgat tttttttcat 3543

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tgctcatgat cctgttactg tgtgccatc atagatttct ttttttagtg ttgcccttgc 3663

tgtgtaataa acgctctatc tagtttacct agcaaaagct caaaactgcg ctagtatgga 3723

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cacgtaagat atatatctgg actctcttgg attataggat ttttcttggc ctgaatatcc 3843

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agttttatct ttagttcaac accatcatgg tggattcatt tataccatct aatatatgac 4083

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<210> 59

<211> 874

<212> PRT

<213> Homo sapiens

<400> 59

Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val Ile Glu Asp His  
   1                  5                  10                  15

Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly His Thr Asn Val  
           20                  25                  30

Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala Pro Lys Pro Gln  
       35                  40                  45

Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly Ser Leu Ala Ser  
 50 55 60  
 Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val Asn Arg Leu Ser  
 65 70 75 80  
 Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn Met Met Ser Ser  
 85 90 95  
 Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser Val Gly Gln Gly  
 100 105 110  
 Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly Gly Asn Ala Pro  
 115 120 125  
 Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln Leu Leu Pro Ser  
 130 135 140  
 Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln Arg Ser Gln Ala  
 145 150 155 160  
 Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser Ser Leu Ser Ser  
 165 170 175  
 Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln Ala Ser Arg Val  
 180 185 190  
 Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala Thr Gly Pro Pro  
 195 200 205  
 Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile Cys Thr Ile Cys  
 210 215 220  
 Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His Phe Glu Lys Glu  
 225 230 235 240  
 His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr Ile Met Lys Ile  
 245 250 255  
 His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg Tyr Leu Pro Thr  
 260 265 270  
 Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu Ser Cys Pro Tyr  
 275 280 285  
 Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala Ala His Met Arg  
 290 295 300  
 Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr Asp Ser Thr Leu  
 305 310 315 320  
 Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr Asn Ile His Leu  
 325 330 335  
 Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala Glu Ser Val Ala  
 340 345 350  
 Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys Pro Gln Pro Lys  
 355 360 365

Val	Gln	Glu	Lys	Ala	Asp	Ile	Pro	Val	Lys	Ser	Ser	Pro	Gln	Ala	Ala		370	375	380
Val	Pro	Tyr	Lys	Lys	Asp	Val	Gly	Lys	Thr	Leu	Cys	Pro	Leu	Cys	Phe		385	390	395
Ser	Ile	Leu	Lys	Gly	Pro	Ile	Ser	Asp	Ala	Leu	Ala	His	His	Leu	Arg		405	410	415
Glu	Arg	His	Gln	Val	Ile	Gln	Thr	Val	His	Pro	Val	Glu	Lys	Lys	Leu		420	425	430
Thr	Tyr	Lys	Cys	Ile	His	Cys	Leu	Gly	Val	Tyr	Thr	Ser	Asn	Met	Thr		435	440	445
Ala	Ser	Thr	Ile	Thr	Leu	His	Leu	Val	His	Cys	Arg	Gly	Val	Gly	Lys		450	455	460
Thr	Gln	Asn	Gly	Gln	Asp	Lys	Thr	Asn	Ala	Pro	Ser	Arg	Leu	Asn	Gln		465	470	475
Ser	Pro	Ser	Leu	Ala	Pro	Val	Lys	Arg	Thr	Tyr	Glu	Gln	Met	Glu	Phe		485	490	495
Pro	Leu	Leu	Lys	Lys	Arg	Lys	Leu	Asp	Asp	Asp	Ser	Asp	Ser	Pro	Ser		500	505	510
Phe	Phe	Glu	Glu	Lys	Pro	Glu	Glu	Pro	Val	Val	Leu	Ala	Leu	Asp	Pro		515	520	525
Lys	Gly	His	Glu	Asp	Asp	Ser	Tyr	Glu	Ala	Arg	Lys	Ser	Phe	Leu	Thr		530	535	540
Lys	Tyr	Phe	Asn	Lys	Gln	Pro	Tyr	Pro	Thr	Arg	Arg	Glu	Ile	Glu	Lys		545	550	555
Leu	Ala	Ala	Ser	Leu	Trp	Leu	Trp	Lys	Ser	Asp	Ile	Ala	Ser	His	Phe		565	570	575
Ser	Asn	Lys	Arg	Lys	Lys	Cys	Val	Arg	Asp	Cys	Glu	Lys	Tyr	Lys	Pro		580	585	590
Gly	Val	Leu	Leu	Gly	Phe	Asn	Met	Lys	Glu	Leu	Asn	Lys	Val	Lys	His		595	600	605
Glu	Met	Asp	Phe	Asp	Ala	Glu	Trp	Leu	Phe	Glu	Asn	His	Asp	Glu	Lys		610	615	620
Asp	Ser	Arg	Val	Asn	Ala	Ser	Lys	Thr	Ala	Asp	Lys	Lys	Leu	Asn	Leu		625	630	635
Gly	Lys	Glu	Asp	Asp	Ser	Ser	Ser	Asp	Ser	Phe	Glu	Asn	Leu	Glu	Glu		645	650	655
Glu	Ser	Asn	Glu	Ser	Gly	Ser	Pro	Phe	Asp	Pro	Val	Phe	Glu	Val	Glu		660	665	670
Pro	Lys	Ile	Ser	Asn	Asp	Asn	Pro	Glu	Glu	His	Val	Leu	Lys	Val	Ile		675	680	685

Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp Gln Lys Glu Asp  
 690 695 700  
 Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu Pro Thr Lys Leu  
 705 710 715 720  
 Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp Asp Val Val Glu  
 725 730 735  
 Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro Gly Ser Gln Gln  
 740 745 750  
 Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys Pro Gly Thr Trp  
 755 760 765  
 Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser Ser Lys Pro Ala  
 770 775 780  
 Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu Gln Leu Lys Trp  
 785 790 795 800  
 Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp Ser Lys Asp Gln  
 805 810 815  
 Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg Leu Ser Asn Pro  
 820 825 830  
 Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu Asp Gly Glu Gln  
 835 840 845  
 Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met His Gly Ser Leu  
 850 855 860  
 Ala Gly Val Lys Leu Ser Ser Gln Gln Ala  
 865 870

<210> 60

<211> 482

<212> DNA

<213> Mus musculus

<220>

<221> promoter

<222> (1)..(482)

<223> mouse activity dependent neurotrophic factor III  
 (ADNF III) promoter

<400> 60

aattgttgagg tgatgagaaa gagagctggt tgccttccgt gttggtcatc aaggtctgcg 60

tgcattgcaa cagtgtcacc tgtgagttcc tgtgtctgaa gccgagaaga tccacaaaat 120

gaggcttttc catagttggt ttgtgttttt aacaagaaaa tggagaggct ttttgtttgt 180

ttttgttttt gtttttttgc ctctgacttc tctctgaaac cagccaacaa gtacaactag 240

caatttttaa agatttagca agaacttgca ctgagttttc atttacagga gcacaaataa 300

aaatatttga ttcaaaaatg catctgagtt cttttaattt ttcctgcagg agaaacctct 360

aaaagtcatt gccttgacaga gtttctggga atgcctgggg gagggagcctg gaacttgtaa 420  
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 tt 482

<210> 61  
 <211> 50  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> H6, H7 and H2 clone human activity dependent  
 neurotrophic factor III (ADNF III) polymorphic  
 region

<220>  
 <221> variation  
 <222> (47)  
 <223> polymorphic site a -> g transition

<400> 61  
 gagttaaact gagcagccaa caggcctaag tgccagggttc cctggcattg 50

<210> 62  
 <211> 50  
 <212> DNA  
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<220>  
 <223> H10 clone human activity dependent neurotrophic  
 factor III (ADNF III) polymorphic region

<220>  
 <221> modified\_base  
 <222> (13)  
 <223> n = unknown

<220>  
 <221> modified\_base  
 <222> (16)  
 <223> n = unknown

<220>  
 <221> modified\_base  
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 <223> n = unknown

<220>  
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 <222> (40)  
 <223> n = unknown

<220>  
 <221> variation  
 <222> (47)  
 <223> polymorphic site a -> g transition

<400> 62  
gagttaaact gancanccan caggcctaag tgccaggtn cctggcggtg 50

<210> 63  
<211> 50  
<212> DNA  
<213> Homo sapiens

<220>  
<223> H3, H12 and H4 clone human activity dependent  
neurotrophic factor III (ADNF III) polymorphic  
region

<220>  
<221> variation  
<222> ()  
<223> polymorphic site a -> g transition

<400> 63  
gagttaaact gagcagccaa caggcctaag tgccaggttc cctggcggtg 50